

SEQUENCE LISTING

<110> Chang, Chawnshang
Yi-Fen Lee
Wen-Jye Lin

<120> Hydroxyflutamide Induced Pathways
Related to Androgen Receptor Negative Prostate Cancer Cells

<130> 21108.0017U2

<140> 10/533,037

<141> 2003-10-31

<150> PCT/US03/34636

<151> 2003-10-31

<150> 60/423,340

<151> 2002-10-31

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1587

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 1

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ctgaaagtcc	atctgctgca	tcggtcaaga	gaaactccac	ttgcatgaag	attgcacgcc	180
tgcagcttgc	atctttgttg	caaaactagc	tacagaagag	aagcaaggca	aagtcttttg	240
tgctccccctc	ccccatcaaa	ggaaagggga	aaatgtctca	gtcgaaaggc	aagaagcgaa	300
accctggcct	taaaattcca	aaagaagcat	ttgaacaacc	tcagaccagt	tccacaccac	360
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tgcggcacgt	gcccagcggg	cagatcatgg	cagtgaagcg	gatccgagcc	acagtaaata	540
gccaggaaca	gaaacggcta	ctgatggatt	tggatatttc	catgaggacg	gtggactgtc	600
cattcactgt	caccttttat	ggcgcaactgt	ttcgggaggg	tgatgtgtgg	atctgcatgg	660
agctcatgga	tacatcacta	gataaattct	acaaacaagt	tattgataaa	ggccagacaa	720
ttccagagga	catcttaggg	aaaatagcag	tttctattgt	aaaagcatta	gaacatttac	780
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aaacaattga	tgcagggtgc	aaaccataca	tggcccctga	aagaataaac	ccagagctca	960
accagaaggg	atacagtgtg	aagtctgaca	tttggagtct	gggcatcacg	atgattgagt	1020
tggccatcct	tcgatttccc	tatgattcat	ggggaactcc	atttcagcag	ctcaaacagg	1080
tggtagagga	gccatcgcca	caactcccag	cagacaagtt	ctctgcagag	tttgttgact	1140
ttacctcaca	gtgctttaaag	aagaattcca	aagaacggcc	tacataacca	gagctaattgc	1200
aacatccatt	tttcacccta	catgaatcca	aagggaacaga	tgtggcatct	tttgtaaaac	1260

tgattcttgg	agactaaaaa	gcagtggact	taatcggttg	accctactgt	ggattgggtgg	1320
gtttcggggg	gaagcaagtt	cactacagca	tcaatagaaa	gtcatctttg	agataattta	1380
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ccttggaatc tatagtatag aatgaactgt ctagatggat gaattatgat aaaggcttag 1500
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<210> 2
<211> 334
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

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 20          25          30
Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
 35          40          45
Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
 50          55          60
Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
 65          70          75          80
Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
 85          90          95
Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
100          105          110
Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
115          120          125
Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
130          135          140
Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
145          150          155          160
Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
165          170          175
His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
180          185          190
Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
195          200          205
Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
210          215          220

Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
225          230          235          240
Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
245          250          255
Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
260          265          270
Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val
275          280          285
Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
290          295          300
Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
305          310          315          320
Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp
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<210> 3
<211> 3080

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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gctactgaca	gcttctcagg	caggttcgaa	gatgtctatc	agctgcagga	ggatgtgctg	180
ggggaagggtg	ctcacgctcg	tgtgcagacc	tgtgtcaatc	tcatacccaa	ccaggaatat	240
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agtgccttgg	acttctctga	taacaaaggc	atcgcccaca	gggacctaaa	gccagagaac	540
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agtggatatca	aactcaatgg	agactgtctc	cccattctcca	caccagagct	gtcaccctcg	660
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<210> 4
 <211> 412
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 20 25 30
 Glu Asp Val Tyr Gln Leu Gln Glu Asp Val Leu Gly Glu Gly Ala His
 35 40 45
 Ala Arg Val Gln Thr Cys Val Asn Leu Ile Thr Asn Gln Glu Tyr Ala
 50 55 60
 Val Lys Ile Ile Glu Lys Gln Leu Gly His Ile Arg Ser Arg Val Phe
 65 70 75 80
 Arg Glu Val Glu Met Leu Tyr Gln Cys Gln Gly His Arg Asn Val Leu
 85 90 95
 Glu Leu Ile Glu Phe Phe Glu Glu Glu Asp Arg Phe Tyr Leu Val Phe
 100 105 110
 Glu Lys Met Arg Gly Gly Ser Ile Leu Ser His Ile His Arg Arg Arg
 115 120 125
 His Phe Asn Glu Leu Glu Ala Ser Val Val Val Gln Asp Val Ala Ser
 130 135 140
 Ala Leu Asp Phe Leu His Asn Lys Gly Ile Ala His Arg Asp Leu Lys
 145 150 155 160
 Pro Glu Asn Ile Leu Cys Glu His Pro Asn Gln Val Ser Pro Val Lys
 165 170 175
 Ile Cys Asp Phe Asp Leu Gly Ser Gly Ile Lys Leu Asn Gly Asp Cys
 180 185 190
 Ser Pro Ile Ser Thr Pro Glu Leu Leu Thr Pro Cys Gly Ser Ala Glu
 195 200 205
 Tyr Met Ala Pro Glu Val Val Glu Ala Phe Ser Glu Glu Ala Ser Ile
 210 215 220
 Tyr Asp Lys Arg Cys Asp Leu Trp Ser Leu Gly Val Ile Leu Tyr Ile
 225 230 235 240
 Leu Leu Ser Gly Tyr Pro Pro Phe Val Gly His Cys Gly Ser Asp Cys
 245 250 255
 Gly Trp Asp Arg Gly Glu Ala Cys Pro Ala Cys Gln Asn Met Leu Phe
 260 265 270
 Glu Ser Ile Gln Glu Gly Lys Tyr Glu Phe Pro Asp Lys Asp Trp Ser
 275 280 285
 His Ile Ser Phe Ala Ala Lys Asp Leu Ile Ser Lys Leu Leu Val Arg
 290 295 300
 Asp Ala Lys Gln Arg Leu Ser Ala Ala Gln Val Leu Gln His Pro Trp
 305 310 315 320
 Val Gln Gly Cys Ala Pro Glu Asn Thr Leu Pro Thr Pro Leu Val Leu
 325 330 335
 Gln Arg Asn Ser Cys Ala Lys Asp Leu Thr Ser Phe Ala Ala Glu Ala
 340 345 350
 Ile Ala Met Asn Arg Gln Leu Ala Gln Cys Glu Glu Asp Ala Gly Gln
 355 360 365
 Asp Gln Pro Val Val Ile Arg Ala Thr Ser Arg Cys Leu Gln Leu Ser
 370 375 380
 Pro Pro Ser Gln Ser Lys Leu Ala Gln Arg Arg Gln Arg Ala Ser Leu
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Ser Ala Thr Pro Val Val Leu Val Gly Asp Arg Ala
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<210> 5
<211> 1096
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

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aaaaaaaaa aaaaaa 1096

<210> 6
<211> 232
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

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20 25 30
Leu Leu Arg Arg Tyr Pro Leu Glu Asp His Pro Glu Phe Pro Leu Pro
35 40 45
Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val Arg
50 55 60
Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr Leu
65 70 75 80
Thr Asp Lys Asp Thr Gly Val Thr Arg Tyr Gly Ile Cys Val Asn Phe
85 90 95
Tyr Arg Ser Phe Gln Lys Arg Met Pro Lys Glu Lys Val Glu Gly Gly
100 105 110
Ala Gly Pro Arg Gly Lys Glu Gly Ala His Thr Ser Gly Ala Ser Glu
115 120 125

Glu	Ala	Ala	Ala	Gly	Ser	Ser	Glu	Ser	Gly	Ser	Thr	Leu	Gln	Pro	Pro
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Ser	Ala	Asp	Ser	Thr	Pro	Asp	Val	Asn	Gln	Ser	Pro	Arg	Gly	Lys	Arg
145					150					155					160
Arg	Ala	Lys	Ala	Gly	Ser	Arg	Ser	Arg	Asn	Ser	Thr	Leu	Thr	Ser	Leu
				165					170					175	
Cys	Val	Leu	Ser	His	Tyr	Pro	Phe	Phe	Ser	Thr	Phe	Arg	Glu	Cys	Leu
			180					185					190		
Tyr	Thr	Leu	Lys	Arg	Leu	Val	Asp	Cys	Cys	Ser	Glu	Arg	Leu	Leu	Gly
	195						200					205			
Lys	Lys	Leu	Gly	Ile	Pro	Arg	Gly	Val	Gln	Arg	Tyr	Gly	Leu	Leu	Leu
	210					215					220				
Val	Leu	Gly	Arg	Thr	Leu	Arg	Asp								
225						230									

<210> 7

<211> 7161

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 7

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<210> 8

<211> 1563

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 8

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Ser Gly Arg Ala Gly Thr Trp Pro Arg Gly Pro Ser Glu Cys Ser Pro
          35          40          45
Arg Glu Lys Met Ala Ala Ala Gly Asn Arg Ala Ser Ser Ser Gly
          50          55          60
Phe Pro Gly Ala Arg Ala Thr Ser Pro Glu Ala Gly Gly Gly Gly Gly
65          70          75          80
Ala Leu Lys Ala Ser Ser Ala Pro Ala Ala Ala Gly Leu Leu Arg
          85          90          95
Glu Ala Gly Ser Gly Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg Gln
          100          105          110

Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln Pro
          115          120          125
Leu Phe Leu Ala Ala Ser Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro
          130          135          140
Glu Pro Ala Asp Ala Ala Gly Ser Gly Thr Gly Phe Gln Pro Val Ala
145          150          155          160
Val Pro Pro Pro His Gly Ala Ala Ser Arg Gly Gly Ala His Leu Thr
          165          170          175

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Glu	Ser	Val	Ala	Ala	Pro	Asp	Ser	Gly	Ala	Ser	Ser	Pro	Ala	Ala	Ala	180	185	190
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			195					200					205					
Ala	Pro	Ala	Gly	Arg	Glu	Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	210	215	220
His	Lys	Met	Asp	Asp	Arg	Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	225	230	235
Lys	Ala	Thr	Cys	Met	Pro	Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Arg	245	250	255
Asn	Arg	Arg	Gly	Pro	Val	Val	Val	Lys	Pro	Ile	Pro	Val	Lys	Gly	Asp	260	265	270
Gly	Ser	Glu	Met	Asn	His	Leu	Ala	Ala	Glu	Ser	Pro	Gly	Glu	Val	Gln	275	280	285
Ala	Ser	Ala	Ala	Ser	Pro	Ala	Ser	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	290	295	300
Gly	Asn	Ser	Pro	Ser	Gly	Arg	Thr	Val	Lys	Ser	Glu	Ser	Pro	Gly	Val	305	310	315
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Pro	Pro	Arg	Arg	Ala	Pro	Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	340	345	350
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Ala	Arg	Gly	Thr	Phe	Cys	Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val	405	410	415
Phe	Gln	Leu	Glu	Pro	Ser	Asp	Pro	Met	Leu	Trp	Arg	Lys	Thr	Leu	Lys	420	425	430
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Glu	Cys	Arg	Arg	Asn	Arg	Glu	Pro	Leu	Ile	Cys	Pro	Leu	Cys	Arg	Ser	530	535	540
Lys	Trp	Arg	Ser	His	Asp	Phe	Tyr	Ser	His	Glu	Leu	Ser	Ser	Pro	Val	545	550	555
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Thr	His	Tyr	Gly	Thr	Gln	Gln	Ile	Pro	Pro	Ala	Tyr	Lys	Asp	Leu	Ala	595	600	605
Glu	Pro	Trp	Ile	Gln	Val	Phe	Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe	610	615	620
Ser	Arg	Asn	Trp	Asn	Val	Arg	Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His	625	630	635
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Asp	Val	Ser	Gly	Ala	Leu	Leu	Leu	Ala	Asn	Gly	Glu	Ser	Thr	Gly	Asn	
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Ser	Gly	Gly	Ser	Ser	Gly	Ser	Ser	Pro	Ser	Gly	Gly	Ala	Thr	Ser	Gly	
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<211> 3621

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<210> 10

<211> 657

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 10

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Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn Ser Ser
          35           40           45
Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala
          50           55           60
Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
65           70           75           80
Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
          85           90           95
Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
          100          105          110
Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
          115          120          125
Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
          130          135          140
Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser
145          150          155          160
Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
          165          170          175
Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg
          180          185          190
Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro
          195          200          205
Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
          210          215          220
Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser
225          230          235          240
Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser
          245          250          255

Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
          260          265          270
Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu
          275          280          285
Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly
          290          295          300
Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser
305          310          315          320

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Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu
 325 330 335
 Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn
 340 345 350
 Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser
 355 360 365
 Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr
 370 375 380
 Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly
 385 390 395 400
 Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly
 405 410 415
 Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro Glu
 420 425 430
 Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys
 435 440 445
 Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp
 450 455 460
 Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly Gly
 465 470 475 480
 Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser Val
 485 490 495
 Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu His
 500 505 510
 Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg
 515 520 525
 Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg
 530 535 540
 Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr Gly
 545 550 555 560
 Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly
 565 570 575
 Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met Leu
 580 585 590
 Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile Phe
 595 600 605
 Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser
 610 615 620
 Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln
 625 630 635 640
 Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu Met
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 Tyr

<210> 11

<211> 3336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

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tgaactcaat catgcaagat ttggctgtcc ttcataaggc cagtcgacca gcattatcct	180
tgcaggaaac cagaaaagca aaatcttcat caccaaaaaa acagaatgat gtccgagtca	240
aatttgaaca tagaggagaa aaaagaatcc ttcagttccc cagaccagtt aaactggaag	300
atctgagatc taaagctaaa attgcctttg gacagtctat ggatctacat tataccaata	360

acgagttggt	aattccatta	actactcaag	atgacttgga	caaagctctg	gaactgctgg	420
atcgtagtat	tcatatgaag	agcctcaaga	tattacttgt	aataaatgga	agtacacagg	480
ctactaattt	agaaccattg	ccatcactag	aagatttgga	taatacagta	tttggagcag	540
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cgggttacat	tccagatgaa	ttacaccagg	ttgcccggaa	tgggtcattc	actagtatca	660
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<210> 12

<211> 544

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 12

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			20					25					30		
Ala	Lys	Ser	Ser	Ser	Pro	Lys	Lys	Gln	Asn	Asp	Val	Arg	Val	Lys	Phe
		35					40					45			
Glu	His	Arg	Gly	Glu	Lys	Arg	Ile	Leu	Gln	Phe	Pro	Arg	Pro	Val	Lys
	50					55					60				
Leu	Glu	Asp	Leu	Arg	Ser	Lys	Ala	Lys	Ile	Ala	Phe	Gly	Gln	Ser	Met
65					70					75					80
Asp	Leu	His	Tyr	Thr	Asn	Asn	Glu	Leu	Val	Ile	Pro	Leu	Thr	Thr	Gln
				85					90					95	
Asp	Asp	Leu	Asp	Lys	Ala	Leu	Glu	Leu	Leu	Asp	Arg	Ser	Ile	His	Met
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Lys	Ser	Leu	Lys	Ile	Leu	Leu	Val	Ile	Asn	Gly	Ser	Thr	Gln	Ala	Thr
		115					120						125		
Asn	Leu	Glu	Pro	Leu	Pro	Ser	Leu	Glu	Asp	Leu	Asp	Asn	Thr	Val	Phe
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Gly	Ala	Glu	Arg	Lys	Lys	Arg	Leu	Ser	Ile	Ile	Gly	Pro	Thr	Ser	Arg
145					150					155					160
Asp	Arg	Ser	Ser	Pro	Pro	Pro	Gly	Tyr	Ile	Pro	Asp	Glu	Leu	His	Gln
				165					170					175	
Val	Ala	Arg	Asn	Gly	Ser	Phe	Thr	Ser	Ile	Asn	Ser	Glu	Gly	Glu	Phe
			180					185					190		
Ile	Pro	Glu	Ser	Met	Glu	Gln	Met	Leu	Asp	Pro	Leu	Ser	Leu	Ser	Ser
	195						200						205		
Pro	Glu	Asn	Ser	Gly	Ser	Gly	Ser	Cys	Pro	Ser	Leu	Asp	Ser	Pro	Leu
	210					215					220				
Asp	Gly	Glu	Ser	Thr	Asp	His	Ser	Leu	Ser	Thr	Ser	Ser	Gly	Ser	Ser
225					230					235					240
Ile	Phe	Thr	Pro	Glu	Tyr	Asp	Asp	Ser	Arg	Ile	Arg	Arg	Arg	Gly	Ser
			245						250					255	
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			260					265					270		
Arg	Ser	Pro	Arg	Ala	Pro	Thr	Asn	Trp	Arg	Leu	Gly	Lys	Leu	Leu	Gly
		275					280					285			
Gln	Gly	Ala	Phe	Gly	Arg	Val	Tyr	Leu	Cys	Tyr	Asp	Val	Asp	Thr	Gly
	290					295					300				
Arg	Glu	Leu	Ala	Val	Lys	Gln	Val	Gln	Phe	Asp	Pro	Asp	Ser	Pro	Glu
305					310					315					320
Thr	Ser	Lys	Glu	Val	Asn	Ala	Leu	Glu	Cys	Glu	Ile	Gln	Leu	Leu	Lys
			325						330					335	
Asn	Leu	Leu	His	Glu	Arg	Ile	Val	Gln	Tyr	Tyr	Gly	Cys	Leu	Arg	Asp
			340					345					350		
Pro	Gln	Glu	Lys	Thr	Leu	Ser	Ile	Phe	Met	Glu	Tyr	Met	Pro	Gly	Gly
	355						360					365			
Ser	Ile	Lys	Asp	Gln	Leu	Lys	Ala	Tyr	Gly	Ala	Leu	Thr	Glu	Asn	Val
	370					375					380				
Thr	Arg	Lys	Tyr	Thr	Arg	Gln	Ile	Leu	Glu	Gly	Val	His	Tyr	Leu	His
385					390					395					400
Ser	Asn	Met	Ile	Val	Leu	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu	Arg
			405						410					415	
Asp	Ser	Thr	Gly	Asn	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ala	Ser	Lys	Arg
			420					425					430		
Leu	Gln	Thr	Ile	Cys	Leu	Ser	Gly	Thr	Gly	Met	Lys	Ser	Val	Thr	Gly
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Thr	Pro	Tyr	Trp	Met	Ser	Pro	Glu	Val	Ile	Ser	Gly	Glu	Gly	Tyr	Gly
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Arg	Lys	Ala	Asp	Ile	Trp	Ser	Val	Ala	Cys	Thr	Val	Val	Glu	Met	Leu
465					470					475					480

Thr	Glu	Lys	Pro	Pro	Trp	Ala	Glu	Phe	Glu	Ala	Met	Ala	Ala	Ile	Phe
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Lys	Ile	Ala	Thr	Gln	Pro	Thr	Asn	Pro	Lys	Leu	Pro	Pro	His	Val	Ser
			500					505					510		
Asp	Tyr	Thr	Arg	Asp	Phe	Leu	Lys	Arg	Ile	Phe	Val	Glu	Ala	Lys	Leu
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Arg	Pro	Ser	Ala	Asp	Glu	Leu	Leu	Arg	His	Met	Phe	Val	His	Tyr	His
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<210> 13
 <211> 444
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 13

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gatgaggtca	tctcgagtgg	cataggtgag	cagagtgtgg	aggggtgaagc	tatggttcaa	360
cagcatttgg	atggtgcctg	aatccacatt	cagttcctgt	agccactgca	ccaggccctg	420
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<210> 14
 <211> 4693
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 14

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gctattatag	aaatggcttg	tgcaaaaacca	ccatggaatg	cagaaaaaca	ctccaatcat	4320
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<210> 15

<211> 1495

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 15

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			20					25					30		
Arg	Glu	Arg	Ala	Asp	Trp	Arg	Arg	Gln	Leu	Arg	Lys	Val	Arg	Ser	
		35				40					45				
Val	Glu	Leu	Asp	Gln	Leu	Pro	Glu	Gln	Pro	Leu	Phe	Leu	Ala	Ala	Ser
	50				55					60					
Pro	Pro	Ala	Ser	Ser	Thr	Ser	Pro	Ser	Pro	Glu	Pro	Ala	Asp	Ala	Ala
65					70					75				80	
Gly	Ser	Gly	Thr	Gly	Phe	Gln	Pro	Val	Ala	Val	Pro	Pro	Pro	His	Gly
				85					90					95	
Ala	Ala	Ser	Arg	Arg	Gly	Ala	His	Leu	Thr	Glu	Ser	Val	Ala	Ala	Pro
			100					105					110		
Asp	Ser	Gly	Ala	Ser	Ser	Pro	Ala	Ala	Ala	Glu	Pro	Gly	Glu	Lys	Arg
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Ala	Pro	Ala	Ala	Glu	Pro	Ser	Pro	Ala	Ala	Ala	Pro	Ala	Gly	Arg	Glu
	130					135					140				
Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	His	Lys	Met	Asp	Asp	Arg
145					150					155					160
Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	Lys	Ala	Thr	Cys	Met	Pro
				165					170					175	
Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Arg	Asn	Arg	Arg	Gly	Pro	Val
			180					185					190		
Val	Val	Lys	Pro	Ile	Pro	Val	Lys	Gly	Asp	Gly	Ser	Glu	Met	Asn	His
		195				200						205			
Leu	Ala	Ala	Glu	Ser	Pro	Gly	Glu	Val	Gln	Ala	Ser	Ala	Ala	Ser	Pro
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Ala	Ser	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	Gly	Asn	Ser	Pro	Ser	Gly
225					230					235					240
Arg	Thr	Val	Lys	Ser	Glu	Ser	Pro	Gly	Val	Arg	Arg	Lys	Arg	Val	Ser
				245					250					255	
Pro	Val	Pro	Phe	Gln	Ser	Gly	Arg	Ile	Thr	Pro	Pro	Arg	Arg	Ala	Pro
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Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	Glu	Glu	Thr	Asn	Arg	Arg
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Val	Asn	Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr	Leu	Leu	Gln	Gln	Ile	Gly
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Pro	Asn	Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser	Pro	Asp	Asn	Lys	Tyr	Arg
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Val	Phe	Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys	Ala	His	Gly	Thr	Phe	Cys
				325					330					335	
Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val	Phe	Gln	Leu	Glu	Pro	Ser
			340					345					350		
Asp	Pro	Met	Leu	Trp	Arg	Lys	Thr	Leu	Lys	Asn	Phe	Glu	Val	Glu	Ser
		355					360					365			
Leu	Phe	Gln	Lys	Tyr	His	Ser	Arg	Arg	Ser	Ser	Arg	Ile	Lys	Ala	Pro
	370					375					380				
Ser	Arg	Asn	Thr	Ile	Gln	Lys	Phe	Val	Ser	Arg	Met	Ser	Asn	Ser	His
385					390					395					400
Thr	Leu	Ser	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Glu	Asn	Ser	Ile
				405					410					415	
Lys	Asp	Glu	Glu	Glu	Gln	Met	Cys	Pro	Ile	Cys	Leu	Leu	Gly	Met	Leu
			420					425					430		

Asp	Glu	Glu	Ser	Leu	Thr	Val	Cys	Glu	Asp	Gly	Cys	Arg	Asn	Lys	Leu	435	440	445
His	His	His	Cys	Met	Ser	Ile	Trp	Ala	Glu	Glu	Cys	Arg	Arg	Asn	Arg	450	455	460
Glu	Pro	Leu	Ile	Cys	Pro	Leu	Cys	Arg	Ser	Lys	Trp	Arg	Ser	His	Asp	465	470	475
Phe	Tyr	Ser	His	Glu	Leu	Ser	Ser	Pro	Val	Asp	Ser	Pro	Ser	Ser	Leu	485	490	495
Arg	Ala	Ala	Gln	Gln	Gln	Thr	Val	Gln	Gln	Gln	Pro	Leu	Ala	Gly	Ser	500	505	510
Arg	Arg	Asn	Gln	Glu	Ser	Asn	Phe	Asn	Leu	Thr	His	Tyr	Gly	Thr	Gln	515	520	525
Gln	Ile	Pro	Pro	Ala	Tyr	Lys	Asp	Leu	Ala	Glu	Pro	Trp	Ile	Gln	Val	530	535	540
Phe	Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe	Ser	Arg	Asn	Trp	Asn	Val	545	550	555
Arg	Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His	Asp	Val	Ser	Gly	Ala	Leu	565	570	575
Leu	Leu	Ala	Asn	Gly	Glu	Ser	Thr	Gly	Asn	Ser	Gly	Gly	Ser	Ser	Gly	580	585	590
Ser	Ser	Pro	Ser	Gly	Gly	Ala	Thr	Ser	Gly	Ser	Ser	Gln	Thr	Ser	Ile	595	600	605
Ser	Gly	Asp	Val	Val	Glu	Ala	Cys	Cys	Ser	Val	Leu	Ser	Met	Val	Cys	610	615	620
Ala	Asp	Pro	Val	Tyr	Lys	Val	Tyr	Val	Ala	Ala	Leu	Lys	Thr	Leu	Arg	625	630	635
Ala	Met	Leu	Val	Tyr	Thr	Pro	Cys	His	Ser	Leu	Ala	Glu	Arg	Ile	Lys	645	650	655
Leu	Gln	Arg	Leu	Leu	Gln	Pro	Val	Val	Asp	Thr	Ile	Leu	Val	Lys	Cys	660	665	670
Ala	Asp	Ala	Asn	Ser	Arg	Thr	Ser	Gln	Leu	Ser	Ile	Ser	Thr	Leu	Leu	675	680	685
Glu	Leu	Cys	Lys	Gly	Gln	Ala	Gly	Glu	Leu	Ala	Val	Gly	Arg	Glu	Ile	690	695	700
Leu	Lys	Ala	Gly	Ser	Ile	Gly	Ile	Gly	Gly	Val	Asp	Tyr	Val	Leu	Asn	705	710	715
Cys	Ile	Leu	Gly	Asn	Gln	Thr	Glu	Ser	Asn	Asn	Trp	Gln	Glu	Leu	Leu	725	730	735
Gly	Arg	Leu	Cys	Leu	Ile	Asp	Arg	Leu	Leu	Leu	Glu	Phe	Pro	Ala	Glu	740	745	750
Phe	Tyr	Pro	His	Ile	Val	Ser	Thr	Asp	Val	Ser	Gln	Ala	Glu	Pro	Val	755	760	765
Glu	Ile	Arg	Tyr	Lys	Lys	Leu	Leu	Ser	Leu	Leu	Thr	Phe	Ala	Leu	Gln	770	775	780
Ser	Ile	Asp	Asn	Ser	His	Ser	Met	Val	Gly	Lys	Leu	Ser	Arg	Arg	Ile	785	790	795
Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Thr	Val	Pro	His	Val	Phe	Ser	805	810	815
Lys	Leu	Leu	Glu	Met	Leu	Ser	Val	Ser	Ser	Val	Ser	Thr	His	Phe	Thr	820	825	830
Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Tyr	Ala	Asp	Glu	Val	Glu	Ile	Ala	835	840	845
Glu	Ala	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Leu	Gln	Arg	Gln	Gln	His	850	855	860
Asn	Ser	Phe	Cys	Arg	His	Leu	Phe	Pro	Thr	Thr	Ile	Trp	Lys	Pro	Gln	865	870	875
Arg	Thr	Val	Pro	Leu	Glu	Cys	Thr	Val	His	Leu	Glu	Lys	Thr	Gly	Lys	885	890	895
Gly	Leu	Cys	Ala	Thr	Lys	Leu	Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Glu	900	905	910

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Pro	His	Ser	Gln	Cys	Leu	Asn	Ser	Ser	Pro	Leu	Ser	His	His	Ser	Gln	945	950	955
Leu	Met	Phe	Pro	Ala	Leu	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Pro	Ser	Val	965	970	975
Pro	Ala	Gly	Thr	Ala	Thr	Asp	Val	Ser	Lys	His	Arg	Leu	Gln	Gly	Phe	980	985	990
Ile	Pro	Cys	Arg	Ile	Pro	Ser	Ala	Ser	Pro	Gln	Thr	Gln	Arg	Lys	Phe	995	1000	1005
Ser	Leu	Gln	Phe	His	Arg	Asn	Cys	Pro	Glu	Asn	Lys	Asp	Ser	Asp	Lys	1010	1015	1020
Leu	Ser	Pro	Val	Phe	Thr	Gln	Ser	Arg	Pro	Leu	Pro	Ser	Ser	Asn	Ile	1025	1030	1035
His	Arg	Pro	Lys	Pro	Ser	Arg	Pro	Thr	Pro	Gly	Asn	Thr	Ser	Lys	Gln	1045	1050	1055
Gly	Asp	Pro	Ser	Lys	Asn	Ser	Met	Thr	Leu	Asp	Leu	Asn	Ser	Ser	Ser	1060	1065	1070
Lys	Cys	Asp	Asp	Ser	Phe	Gly	Leu	Ser	Ser	Asn	Ser	Ser	Asn	Cys	Cys	1075	1080	1085
Tyr	Thr	Ser	Asp	Glu	Thr	Val	Phe	Thr	Pro	Val	Glu	Glu	Lys	Cys	Arg	1090	1095	1100
Leu	Asp	Val	Asn	Thr	Glu	Leu	Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	1105	1110	1115
Ala	Ser	Met	Pro	Ser	Ser	Asp	Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	1125	1130	1135
Ala	Val	Leu	Ser	Pro	Glu	Lys	Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	1140	1145	1150
Asp	Val	Asn	His	Asn	Gln	Lys	Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	1155	1160	1165
Glu	Glu	Ala	Leu	Ala	Ile	Ala	Met	Ala	Met	Ser	Ala	Ser	Gln	Val	Ala	1170	1175	1180
Leu	Pro	Ile	Val	Pro	Gln	Leu	Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	1185	1190	1195
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Ser	Glu	Gln	Glu	Glu	Val	Val	Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	1265	1270	1275
Met	Ser	His	Leu	Asn	His	Pro	Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	1285	1290	1295
Cys	Glu	Lys	Ser	Asn	Tyr	Asn	Leu	Phe	Ile	Glu	Trp	Met	Ala	Gly	Gly	1300	1305	1310
Ser	Val	Ala	His	Leu	Leu	Ser	Lys	Tyr	Gly	Ala	Phe	Lys	Glu	Ser	Val	1315	1320	1325
Val	Ile	Asn	Tyr	Thr	Glu	Gln	Leu	Leu	Arg	Gly	Leu	Ser	Tyr	Leu	His	1330	1335	1340
Glu	Asn	Gln	Ile	Ile	His	Arg	Asp	Val	Lys	Gly	Ala	Asn	Leu	Leu	Ile	1345	1350	1355
Asp	Ser	Thr	Gly	Gln	Arg	Leu	Arg	Ile	Ala	Asp	Phe	Gly	Ala	Ala	Ala	1365	1370	1375
Arg	Leu	Ala	Ser	Lys	Gly	Thr	Gly	Ala	Gly	Glu	Phe	Gln	Gly	Gln	Leu	1380	1385	1390

Leu Gly Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln
 1395 1400 1405
 Tyr Gly Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu
 1410 1415 1420
 Met Ala Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His
 1425 1430 1435 1440
 Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile
 1445 1450 1455
 Pro Ser His Leu Ser Pro Gly Leu Arg Asp Val Ala Leu Arg Cys Leu
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 Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His
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 Pro Val Phe Arg Thr Thr Trp
 1490 1495

<210> 16
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 16
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37

<210> 17
 <211> 2348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

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 ggcgccgtgc gagtgccgac agcgagaatg ccctctctgt gcaggagagg aatgtgccaa 1140
 ccaagtctcc cagtgcctcc atcaactggc gccggggaaa gctcctgggc cagggtgcct 1200
 tcggcagggt ctatttgtgc tatgacgtgg acacgggacg tgaacttgct tccaagcagg 1260
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 accgcgctga gaagaccctg accatcttca tggagtacat gccagggggc tcggtgaaag 1440

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accagttgaa ggcttacggt gctctgacag agagcgtgac ccgaaagtac acgcggcaga 1500
tcctggaggg catgtcctac ctgcacagca acatgattgt tcaccgggac attaagggag 1560
ccaacatcct ccgagactct gctgggaatg taaagctggg ggactttggg gccagcaaac 1620
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ccccagcctg tcagatccag gagctccagt gtcttgagct cagcgtggag gggtaggggc 2220
tggaacaggt gtgcaaggca gccgtgggcc ccaccctcgg ggatgtgtcc tgacactgca 2280
attggcaccg aagcccagag ggtctggggg cacaagactg acgccagggt atgaagagtg 2340
ttatttttc
2348

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<210> 18

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

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1          5          10          15
Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys
20         25         30
Asn Lys Asp Thr Gly His Ser Asn Arg Gln Ser Asp Val Arg Ile Lys
35         40         45
Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val
50         55         60
Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro
65         70         75         80
Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn
85         90         95
Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser
100        105        110
Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn
115        120        125
Ser Ser Ser Pro His Ser Glu Val Ser Arg Gln Val Arg Ile Lys Ala
130        135        140
Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro
145        150        155        160
Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser
165        170        175
Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln
180        185        190
Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr
195        200        205
Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu
210        215        220
Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe
225        230        235        240
Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln
245        250        255
Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly
260        265        270

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Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr
 275 280 285
 Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn
 290 295 300
 Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu
 305 310 315 320
 Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg
 325 330 335
 Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro
 340 345 350
 Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu
 355 360 365
 Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr
 370 375 380
 Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro
 385 390 395 400
 Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu
 405 410 415
 Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg
 420 425 430
 Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly
 435 440 445
 Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser
 450 455 460
 Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu
 465 470 475 480
 His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu
 485 490 495
 Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys
 500 505 510
 Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr
 515 520 525
 Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr
 530 535 540
 Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met
 545 550 555 560
 Leu Thr Glu Lys Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile
 565 570 575
 Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile
 580 585 590
 Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg
 595 600 605
 Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu
 610 615 620
 Met Tyr
 625

<210> 19

<211> 1576

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 19

gaattcgagc	cgaccgaccg	ctcccggccc	gccccctatg	ggccccggct	agaggcgccg	60
ccgccgcccg	cccgcggagc	cccgatgctg	gcccggagga	agccggtgct	gccggcgctc	120
accatcaacc	ctaccatcgc	cgagggccca	tcccctacca	gcgagggcgc	ctccgaggca	180

aacctgggtgg	acctgcagaa	gaagctggag	gagctggaac	ttgacgagca	gcagaagaag	240
cggctggaag	cctttctcac	ccagaaagcc	aagggtggcg	aactcaaaga	cgatgacttc	300
gaaaggatct	cagagctggg	cgcgggcaac	ggcggggtag	tcaccaaagt	ccagcacaga	360
ccctcggggc	tcatcatggc	caggaagctg	atccaccttg	agatcaagcc	ggccatccgg	420
aaccagatca	tccgcgagct	gcaggtcctg	cacgaatgca	actcgcgcta	catcgtgggc	480
ttctacgggg	ccttctacag	tgacggggag	atcagcattt	gcatggaaca	catggacggc	540
ggctccctgg	accaggtgct	gaaagaggcc	aagaggattc	ccgaggagat	cctggggaaa	600
gtcagcatcg	cggttctccg	gggcttggcg	tacctccgag	agaagcacca	gatcatgcac	660
cgagatgtga	agccctccaa	catcctcgtg	aactctagag	gggagatcaa	gctgtgtgac	720
ttcgggggtga	gcggccagct	catagactcc	atggccaact	ccttcgtggg	cacgcgctcc	780
tacatggctc	cggagcgggt	gcagggcaca	cattactcgg	tgacgtcgga	catctggagc	840
atgggctgt	cctgggtgga	gctggccgtc	ggaaggtagc	ccatcccccc	gcccagcgcc	900
aaagagctgg	agcccatctt	tggccggccc	gtggtcgacg	gggaagaagg	agagcctcac	960
agcatctcgc	ctcggccgag	gccccccggg	cgccccgtca	gcggtcacgg	gatggatagc	1020
cggcctgcca	tggccatctt	tgaactcctg	gactatattg	tgaacgagcc	acctcctaag	1080
ctgcccacag	gtgtgttcac	ccccgacttc	caggagtttg	tcaataaatg	cctcatcaag	1140
aaccacagcg	agcggggcga	cctgaagatg	ctcacaaaac	acaccttcac	caagcggctc	1200
gaggtggaag	aagtggattt	tgccggctgg	ttgtgtaaaa	ccctgcggct	gaaccagccc	1260
ggcacaccca	cgcgcaccgc	cgtgtgacag	tgccggggct	ccctgcgtcc	cgctgggtgac	1320
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cacctctctg	cctcaccttg	cggagagcac	cgtggcgggg	cgacagcgca	tgacggaacg	1440
gggggtctct	ctcctgccag	tcctggccgg	ggtgcctctg	gggacggggc	acgctgctgt	1500
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aaaaaaaaaa	aaaaaa					1576

<210> 20

<211> 2222

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 20

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cccgggtcca	aaatgcccaa	gaagaagccg	acgcccaccc	agctgaaccc	ggcccccgac	120
ggctctgcag	ttaacgggac	cagctctgcg	gagaccaact	tggaggcctt	gcagaagaag	180
ctggaggagc	tagagcttga	tgagcagcag	cgaaagcgcc	ttgaggcctt	tcttaccag	240
aagcagaagg	tgggagaact	gaaggatgac	gactttgaga	agatcagtga	gctgggggct	300
ggcaatggcg	gtgtggtggt	caaggtctcc	cacaagcctt	ctggcctggt	catggccaga	360
aagctaattc	atctggagat	caaaccgcga	atccgggaac	agatcataag	ggagctgcag	420
gttctgcatg	agtgcactc	tccgtacatc	gtgggcttct	atgggtgcgt	ctacagcgat	480
ggcgagatca	gtatctgcat	ggagcacatg	gatggagggt	ctctggatca	agtccctgaag	540
aaagctggaa	gaattcctga	acaaatttta	ggaaaagtta	gcattgctgt	aataaaaaggc	600
ctgacataat	tgaggggagaa	gcacaagatc	atgcacagag	atgtcaagcc	ctccaacatc	660
ctagtcaact	cccggtggga	gatcaagctc	tgtgactttg	gggtcagcgg	gcagctcatc	720
gactccatgg	ccaactcctt	cgtgggcaca	aggtcctaca	tgtcgccaga	aagactccag	780
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tgccagggtg	aaggagatgc	ggctgagacc	ccaccagggc	caaggacccc	cgggaggccc	960
cttagctcat	acggaatgga	cagccgacct	cccatggcaa	tttttgagtt	gttggtattac	1020
atagtcaacg	agcctcctcc	aaaactgccc	agtggagtg	tcagtctgga	atttcaagat	1080
tttctgaata	aatgcttaat	aaaaaacccc	gcagagagag	cagatttgaa	gcaactcatg	1140
gttcatgctt	ttatcaagag	atctgatgct	gaggaagtgg	attttgcagg	ttggctgtgc	1200
tccaccatcg	gccttaacca	gcccagcaca	ccaaccatg	ctgctggcgt	ctaagtgttt	1260
gggaagcaac	aaagagcgag	tcccctgccc	ggtgggtttg	catgtcgctt	ttgggcctcc	1320
ttcccatgcc	tgtctctggt	cagatgtgca	tttcacctgt	gacaaaggat	gaagaacaca	1380
gcatgtgcca	agattctact	cttgtcattt	ttaatattac	tgtctttatt	cttattacta	1440
ttattgttcc	cctaagtgga	ttggctttgt	gcttgggggt	atttgtgtgt	atgctgatga	1500
tcaaaacctg	tgccaggctg	aattacagtg	aaatttttgg	tgaatgtggg	tagtcattct	1560

tacaattgca	ctgctgttcc	tgtcccatga	ctggctgtct	gcctgtattt	tcggactttg	1620
acatttgaca	tttgggtggac	tttatcttgc	tgggcatact	ttctctctag	gagggagcct	1680
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aaccatttta	acctagatgt	ttaacaaatc	taatctctta	ttctaataaa	tatactatga	2160
aataaaaaaa	aaaggagaaa	gctaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2220
aa						2222

<210> 21

<211> 2371

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 21

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gcaagaagcc	gagcccagag	ggcggccgcg	accctcttga	ccgagatcct	gctgcttttcg	120
agccaggagc	accgtcccctc	cccggattag	tgcgtacgag	cgcccagtg	cctggcccgcg	180
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aggaaaactgg	ggagtcttga	gggacccccg	actccaagcg	cgaaaacccc	ggatgggtgag	300
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acagattcca	gcttcggaac	aagagaccct	ggttagacca	aagccattgc	ttttgaagtt	420
attaaagtct	gttgggtgcac	aaaaagacac	ttatactatg	aaagagggtc	ttttttatct	480
tggccagtat	attatgacta	aacgattata	tgatgagaag	caacaacata	ttgtatatgt	540
ttcaaagtga	cttctaggag	atttgtttgg	cgtgccaagc	ttctctgtga	aagagcacag	600
gaaaatatat	accatgatct	acaggaactt	ggtagtagtc	aatcagcagg	aatcatcgga	660
ctcagggtaca	tctgtgagtg	agaacagggtg	tcaccttgaa	ggtggggagtg	atcaaaaagga	720
ccttgtacaa	gagcttcagg	aagagaaacc	ttcatcttca	catttggttt	ctagaccatc	780
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tgaacgacaa	agaaaacgcc	acaaatctga	tagtatttcc	ctttcccttg	atgaaagcct	900
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gacgccatcg	aatccggatc	ttgatgctgg	tgtaaagtga	cattcagggtg	attgggttga	1020
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ttccttagct	gactattgga	aatgcacttc	atgcaatgaa	atgaatcccc	cccttccatc	1260
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tcttatggcc	tgtcttacat	gtgcaaagaa	gctaaagaaa	aggaataagc	cctgcccagt	1740
atgtagacaa	ccaattcaaa	tgattgtgct	aacttatctc	ccctagtgtg	cctgtctata	1800
agagaattat	atatttctaa	ctatataaac	ctaggaattt	agacaacctg	aaatttatct	1860
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gaccgagtct	tgtctgtgta	cccaggctgg	agtgcagtg	gtgatcttgg	ctcactgcaa	2160
gctctgccct	cccgggttc	gcaccattct	cctgcctcag	cctcccaatt	agcttggcct	2220
acagtcacat	gccaccacac	ctggctaatt	ttttgtactt	ttagtagaga	cagggtttca	2280

ccgtgttagc caggatggtc tcgatctcct gacctcgtga tccgcccacc tcggcctccc
 aaagtgtggtg gattacaggc atgagccacc g

2340

2371

<210> 22

<211> 491

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 22

Met	Cys	Asn	Thr	Asn	Met	Ser	Val	Pro	Thr	Asp	Gly	Ala	Val	Thr	Thr
1				5					10					15	
Ser	Gln	Ile	Pro	Ala	Ser	Glu	Gln	Glu	Thr	Leu	Val	Arg	Pro	Lys	Pro
			20					25					30		
Leu	Leu	Leu	Lys	Leu	Leu	Lys	Ser	Val	Gly	Ala	Gln	Lys	Asp	Thr	Tyr
		35					40					45			
Thr	Met	Lys	Glu	Val	Leu	Phe	Tyr	Leu	Gly	Gln	Tyr	Ile	Met	Thr	Lys
	50					55					60				
Arg	Leu	Tyr	Asp	Glu	Lys	Gln	Gln	His	Ile	Val	Tyr	Cys	Ser	Asn	Asp
65					70					75				80	
Leu	Leu	Gly	Asp	Leu	Phe	Gly	Val	Pro	Ser	Phe	Ser	Val	Lys	Glu	His
			85					90					95		
Arg	Lys	Ile	Tyr	Thr	Met	Ile	Tyr	Arg	Asn	Leu	Val	Val	Val	Asn	Gln
			100					105					110		
Gln	Glu	Ser	Ser	Asp	Ser	Gly	Thr	Ser	Val	Ser	Glu	Asn	Arg	Cys	His
		115					120					125			
Leu	Glu	Gly	Gly	Ser	Asp	Gln	Lys	Asp	Leu	Val	Gln	Glu	Leu	Gln	Glu
	130					135					140				
Glu	Lys	Pro	Ser	Ser	Ser	His	Leu	Val	Ser	Arg	Pro	Ser	Thr	Ser	Ser
145					150					155				160	
Arg	Arg	Arg	Ala	Ile	Ser	Glu	Thr	Glu	Glu	Asn	Ser	Asp	Glu	Leu	Ser
			165					170					175		
Gly	Glu	Arg	Gln	Arg	Lys	Arg	His	Lys	Ser	Asp	Ser	Ile	Ser	Leu	Ser
		180					185					190			
Phe	Asp	Glu	Ser	Leu	Ala	Leu	Cys	Val	Ile	Arg	Glu	Ile	Cys	Cys	Glu
	195					200					205				
Arg	Ser	Ser	Ser	Ser	Glu	Ser	Thr	Gly	Thr	Pro	Ser	Asn	Pro	Asp	Leu
	210					215					220				
Asp	Ala	Gly	Val	Ser	Glu	His	Ser	Gly	Asp	Trp	Leu	Asp	Gln	Asp	Ser
225					230				235					240	
Val	Ser	Asp	Gln	Phe	Ser	Val	Glu	Phe	Glu	Val	Glu	Ser	Leu	Asp	Ser
			245					250					255		
Glu	Asp	Tyr	Ser	Leu	Ser	Glu	Glu	Gly	Gln	Glu	Leu	Ser	Asp	Glu	Asp
		260					265					270			
Asp	Glu	Val	Tyr	Gln	Val	Thr	Val	Tyr	Gln	Ala	Gly	Glu	Ser	Asp	Thr
	275					280					285				
Asp	Ser	Phe	Glu	Glu	Asp	Pro	Glu	Ile	Ser	Leu	Ala	Asp	Tyr	Trp	Lys
	290				295						300				
Cys	Thr	Ser	Cys	Asn	Glu	Met	Asn	Pro	Pro	Leu	Pro	Ser	His	Cys	Asn
305					310					315				320	
Arg	Cys	Trp	Ala	Leu	Arg	Glu	Asn	Trp	Leu	Pro	Glu	Asp	Lys	Gly	Lys
			325					330					335		
Asp	Lys	Gly	Glu	Ile	Ser	Glu	Lys	Ala	Lys	Leu	Glu	Asn	Ser	Thr	Gln
		340					345					350			
Ala	Glu	Glu	Gly	Phe	Asp	Val	Pro	Asp	Cys	Lys	Lys	Thr	Ile	Val	Asn
	355					360					365				
Asp	Ser	Arg	Glu	Ser	Cys	Val	Glu	Glu	Asn	Asp	Asp	Lys	Ile	Thr	Gln

370	375	380
Ala Ser Gln Ser Gln Glu Ser Glu Asp Tyr Ser Gln Pro Ser Thr Ser		
385	390	400
Ser Ser Ile Ile Tyr Ser Ser Gln Glu Asp Val Lys Glu Phe Glu Arg		
	405	415
Glu Glu Thr Gln Asp Lys Glu Glu Ser Val Glu Ser Ser Leu Pro Leu		
	420	430
Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro Lys Asn Gly		
	435	445
Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys Phe Thr Cys		
	450	460
Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln		
465	470	480
Pro Ile Gln Met Ile Val Leu Thr Tyr Phe Pro		
	485	490

<210> 23
 <211> 1599
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 23

gagactgtgc	cctgtccacg	gtgcctcctg	catgtcctgc	tgccctgagc	tgtcccagagc	60
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ctccacaagc	gtggtgaata	catcaagacc	tggaggccac	ggtagcttct	gctgaagagc	180
gacggctcct	tcattgggta	caaggagagg	cccaggcccc	ctgatcagac	tctaccccc	240
ttaaacaact	tctccgtagc	agaatgccag	ctgatgaaga	ccgagaggcc	gcgacccaac	300
acctttgtca	tacgctgcct	gcagtggacc	acagtcacgc	agaggacctt	ccacgtggat	360
tctccagacg	agagggagga	gtggatgcgg	gccatccaga	tggctcgcaa	cagcctcaag	420
cagcggggccc	caggcgagga	ccccatggac	tacaagtgtg	gctccccccag	tgactcctcc	480
acgactgagg	agatggaagt	ggcggtcagc	aaggcacggg	ctaaagtgac	catgaatgac	540
ttcgactatc	tcaaactcct	tggcaaggga	acctttggca	aagtcatcct	ggtgcgggag	600
aaggccactg	gccgctacta	cgccatgaag	atcctgcgaa	aggaagtcac	cattgccaag	660
gatgaagtgc	ctcacacagt	caccgagagc	cgggtcctcc	agaacaccag	gcacccgttc	720
ctcactgcgc	tgaagtatgc	cttcacagac	cacgaccgcc	tgtgctttgt	gatggagtat	780
gccaacgggg	gtgagctggt	cttcacacct	tcccgggagc	gtgtcttcac	agaggagcgg	840
gcccggtttt	atggtgcaga	gattgtctcg	gctcttgagt	acttgcactc	gcgggacgtg	900
gtataccgcg	acatcaagct	ggaaaacctc	atgctggaca	aagatggcca	catcaagatc	960
actgactttg	gcctctgcaa	agagggcatc	agtgcggggg	ccaccatgaa	aaccttctgt	1020
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gactggtggg	ggctgggtgt	ggtcatgtac	gagatgatgt	gcggccgcct	gcccttctac	1140
aaccaggacc	acgagcgctt	cttcgagctc	atcctcatgg	aagagatccg	cttcccgcgc	1200
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tccgaggtcg	acacaaggta	cttcgatgat	gaatttaccg	cccagtccat	cacaatcaca	1440
ccccctgacc	gctatgacag	cctgggctta	ctggagctgg	accagcggac	ccacttcccc	1500
cagttctcct	actcggccag	catccgcgag	tgagcagttc	gcccacgcag	aggacgcacg	1560
ctcgtgcca	tcaccgctgg	gtggtttttt	accctgcc			1599

<210> 24
 <211> 481
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =

synthetic construct

<400> 24

Met	Asn	Glu	Val	Ser	Val	Ile	Lys	Glu	Gly	Trp	Leu	His	Lys	Arg	Gly
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Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	Tyr	Phe	Leu	Leu	Lys	Ser	Asp
			20					25					30		
Gly	Ser	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	Pro	Glu	Ala	Pro	Asp	Gln	Thr
		35				40						45			
Leu	Pro	Pro	Leu	Asn	Asn	Phe	Ser	Val	Ala	Glu	Cys	Gln	Leu	Met	Lys
	50				55						60				
Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	Val	Ile	Arg	Cys	Leu	Gln	Trp
65					70					75					80
Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Asp	Ser	Pro	Asp	Glu	Arg
				85					90					95	
Glu	Glu	Trp	Met	Arg	Ala	Ile	Gln	Met	Val	Ala	Asn	Ser	Leu	Lys	Gln
			100					105					110		
Arg	Ala	Pro	Gly	Glu	Asp	Pro	Met	Asp	Tyr	Lys	Cys	Gly	Ser	Pro	Ser
		115					120					125			
Asp	Ser	Ser	Thr	Thr	Glu	Glu	Met	Glu	Val	Ala	Val	Ser	Lys	Ala	Arg
	130					135					140				
Ala	Lys	Val	Thr	Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys
145					150					155					160
Gly	Thr	Phe	Gly	Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Thr	Gly	Arg
				165					170					175	
Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp
		180						185					190		
Glu	Val	Ala	His	Thr	Val	Thr	Glu	Ser	Arg	Val	Leu	Gln	Asn	Thr	Arg
	195						200					205			
His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ala	Phe	Gln	Thr	His	Asp	Arg
	210					215					220				
Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His
225					230					235					240
Leu	Ser	Arg	Glu	Arg	Val	Phe	Thr	Glu	Glu	Arg	Ala	Arg	Phe	Tyr	Gly
				245					250					255	
Ala	Glu	Ile	Val	Ser	Ala	Leu	Glu	Tyr	Leu	His	Ser	Arg	Asp	Val	Val
			260					265					270		
Tyr	Arg	Asp	Ile	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His
	275						280					285			
Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Ser	Asp	Gly
	290					295					300				
Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu
305					310					315					320
Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu
				325					330					335	
Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn
			340					345					350		
Gln	Asp	His	Glu	Arg	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg
	355						360					365			
Phe	Pro	Arg	Thr	Leu	Ser	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ala	Gly	Leu
	370					375					380				
Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Pro	Ser	Asp	Ala
385					390					395					400
Lys	Glu	Val	Met	Glu	His	Arg	Phe	Phe	Leu	Ser	Ile	Asn	Trp	Gln	Asp
				405					410					415	
Val	Val	Gln	Lys	Lys	Leu	Leu	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser
			420					425					430		
Glu	Val	Asp	Thr	Arg	Tyr	Phe	Asp	Asp	Glu	Phe	Thr	Ala	Gln	Ser	Ile
	435						440					445			
Thr	Ile	Thr	Pro	Pro	Asp	Arg	Tyr	Asp	Ser	Leu	Gly	Leu	Leu	Glu	Leu
	450					455					460				

Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg
 465 470 475 480
 Glu

<210> 25
 <211> 1547
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 25
 gggagtcattc atgagcgatg ttaccattgt gaaagaagggt tgggttcaga agaggggaga 60
 atatataaaa aactggaggc caagatactt ccttttgaag acagatggct cattcatagg 120
 atataaagag aaacctcaag atgtggattt accttatccc ctcaacaact tttcagtggc 180
 aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct 240
 ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaagggaga 300
 atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat 360
 gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac 420
 aacccatcat aaaagaaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg 480
 cacttttggg aaagtatttt tgggttcaga gaaggcaagt ggaaaatact atgctatgaa 540
 gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag 600
 cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttccagac 660
 aaaagaccgt ttgtgttttg tgatggaata tgtaaatggg ggcgagctgt ttttccattt 720
 gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc 780
 tgccctggac tatctacatt ccggaagat tgtgtaccgt gatctcaagt tggagaatct 840
 aatgctggac aaagatggcc acataaaaaat tacagatttt ggactttgca aagaaggat 900
 cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagagg 960
 gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta 1020
 tgaaatgatg tgtgggagggt tacctttcta caaccaggac catgagaaac tttttgaatt 1080
 aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct 1140
 ttcagggctc ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa 1200
 agaaattatg agacacagtt tcttctctgg agtaaactgg caagatgtat atgataaaaa 1260
 gcttgtacct ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga 1320
 agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggat 1380
 ggactgcatg gacaatgaga ggcgccgca tttccctcaa ttttccctact ctgcaagtgg 1440
 acgagaataa gtctctttca ttctgctact tcaactgtcat cttcaattta ttactgaaaa 1500
 tgattcctgg acatcaccag tcctagctct tacacatagc aggggca 1547

<210> 26
 <211> 479
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 26
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 Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
 20 25 30
 Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
 35 40 45
 Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
 50 55 60

Glu	Arg	Pro	Lys	Pro	Asn	Thr	Phe	Ile	Ile	Arg	Cys	Leu	Gln	Trp	Thr	65	70	75	80
Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Asp	Thr	Pro	Glu	Glu	Arg	Glu	85	90	95	
Glu	Trp	Thr	Glu	Ala	Ile	Gln	Ala	Val	Ala	Asp	Arg	Leu	Gln	Arg	Gln	100	105	110	
Glu	Glu	Glu	Arg	Met	Asn	Cys	Ser	Pro	Thr	Ser	Gln	Ile	Asp	Asn	Ile	115	120	125	
Gly	Glu	Glu	Glu	Met	Asp	Ala	Ser	Thr	Thr	His	His	Lys	Arg	Lys	Thr	130	135	140	
Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	145	150	155	160
Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Tyr	Ala	Met	165	170	175	
Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	Glu	Val	Ala	His	180	185	190	
Thr	Leu	Thr	Glu	Ser	Arg	Val	Leu	Lys	Asn	Thr	Arg	His	Pro	Phe	Leu	195	200	205	
Thr	Ser	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	Lys	Asp	Arg	Leu	Cys	Phe	Val	210	215	220	
Met	Glu	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	225	230	235	240
Arg	Val	Phe	Ser	Glu	Asp	Arg	Thr	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	245	250	255	
Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Gly	Lys	Ile	Val	Tyr	Arg	Asp	Leu	260	265	270	
Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	275	280	285	
Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Thr	Asp	Ala	Ala	Thr	Met	Lys	290	295	300	
Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	305	310	315	320
Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	325	330	335	
Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	340	345	350	
Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Asp	Ile	Lys	Phe	Pro	Arg	Thr	355	360	365	
Leu	Ser	Ser	Asp	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Ile	Lys	Asp	370	375	380	
Pro	Asn	Lys	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	Glu	Ile	Met	385	390	395	400
Arg	His	Ser	Phe	Phe	Ser	Gly	Val	Asn	Trp	Gln	Asp	Val	Tyr	Asp	Lys	405	410	415	
Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	420	425	430	
Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Thr	Ile	Thr	Ile	Thr	Pro	435	440	445	
Pro	Glu	Lys	Tyr	Asp	Glu	Asp	Gly	Met	Asp	Cys	Met	Asp	Asn	Glu	Arg	450	455	460	
Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Gly	Arg	Glu		465	470	475	

<210> 27

<211> 2277

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 27

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gcgaggcgag cgcggggaag gcaggccggc agcccgtgtg agcccatgc ggcgagcgcc      120
tgcgagaagg ggaggaggag ccggcccgcc gcccgccgcc cggggatggt gaggaggcgg      180
cgctgcgtga gcccagttag gccttcgctc gggcccgccg ccagctctcc cttcctccgc      240
tcgctcgctc ccccttccc tctcctccc tgccgcgcc gccgcgcc tcccatcacc      300
tctccccgg gctcccgag ccataagtag ctgagaagga gaaagacaag aaaaagaaca      360
tcccttttgt ggacccttct gctggagttc aggaatttca acggtgatct tttgactgat      420
ccaccagcct gataaactga tccaccaaga gacattcccg ccattatgaa tgaagtagcg      480
atagtgaagg aaggatggct ccacaaacga ggagaatata tcaaaacatg gaggccacgg      540
tattttcttt taaagaatga tggcacattc attggctaca aggaacgacc gcaagacggt      600
gaccaacgag aatcaccttt aaataacttc tcagtagctc agtgccagct gatgaagaca      660
gaacgaccta aaccaaacac atttatcatt agatgcctcc agtggaccac agtaattgaa      720
agaacatttc atgtggagac tccagaggag cgggaagaat ggacaaaagc tatccaaact      780
gttgacagaca gcctcaagaa acaggaggaa gagatgatgg atttttagatc tggttctcct      840
agtgataatt caggtgctga agaaatggaa gtttctatga caaagccaaa acacaaagtg      900
accatgaatg aatttgaata ccttaagcta ctgggaaaag gcacttttgg aaaggtcatt      960
ttagttaaag aaaaagcaac cggacggtat tatgctatga aaattctgaa gaaggaagtt     1020
attgtagcaa aggatgaagt agcacacacg ctgacagaaa accgtgtttt acagaactca     1080
cggcatccat tcttaacagc tttaaagtat tcctttcaga cacacgatcg cttgtgtttt     1140
gttatggagt atgctaacgg aggggagttg tttttccatc tgtcgagaga gcgtgtattt     1200
tctgaagacc gggcgcggtt ttatggggct gagattgttt cagcgctgga ttacctgcat     1260
tcagagaaga atgtggtgta cagagatttg aagctggaaa atcttatgct ggataaagac     1320
gggcacataa aaattacaga ctttgacta tgtaaagaag gcataaaaga tggagcaaca     1380
atgaagactt tctgtggcac tccagagtat cttgcaccag aggtgctgga ggataatgac     1440
tatggtcgtg cagtggactg gtggggatta ggagttgtga tgtatgaaat gatgtgtggc     1500
cggctccctt tctacaatca ggaccatgaa aagctctttg aactcatcct tatggaagag     1560
attagatttc cagcaccttt gtcacctgaa gcaaaatctc tcttgtcagg tttgctgaag     1620
aaagatccta agcaaaaggt aggagcggt cctgatgatg ccaaggagat tatgcagcac     1680
aaattctttg ctggcattgt ttggcaagat gtatacggga agaagcttgt acctccattt     1740
aagccacaag ttacatctga aacagataca agatactttg atgaagaatt tacagcacag     1800
atgattacaa tctactcctc tgaccaagat gacagcatgg attgtgtaga caatgagaga     1860
agacctcatt ttcctcagtt ctctattca gccagtggaa ccgcttaatg ttttgacgtg     1920
ttttcccat cagaaacaaa acagactgca ttttggggac cttacttcaa tggacactag     1980
agaactttct atattatctg aattacaaac tgtgtttgta ttacgattta gatgaatttc     2040
taggaagcct cacagattct gtatttaaaa caattctttg atgcattttt gagaaggaaa     2100
acaaatccat tcttaagata ttacgtcaag gctcttatgc tgaacgacca taggttttta     2160
agaatatgca ccaaaactgt ttactttaga attaatgaag gcattcaata tcagctatag     2220
gatctaataca ttcctgtcaa aagtttaaga ccaggaacct tagagtagaa acgaaac      2277

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<210> 28

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 28

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Met Asn Glu Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
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Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
              20              25              30
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
              35              40              45
Glu Ser Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
              50              55              60
Thr Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
65              70              75              80

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Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Glu	Thr	Pro	Glu	Glu	Arg	85	90	95
Glu	Glu	Trp	Thr	Lys	Ala	Ile	Gln	Thr	Val	Ala	Asp	Ser	Leu	Lys	Lys	100	105	110
Gln	Glu	Glu	Glu	Met	Met	Asp	Phe	Arg	Ser	Gly	Ser	Pro	Ser	Asp	Asn	115	120	125
Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser	Met	Thr	Lys	Pro	Lys	His	Lys	130	135	140
Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	145	150	155
Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	165	170	175
Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Val	Ala	Lys	Asp	Glu	Val	180	185	190
Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	Leu	Gln	Asn	Ser	Arg	His	Pro	195	200	205
Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	His	Asp	Arg	Leu	Cys	210	215	220
Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	225	230	235
Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	245	250	255
Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Glu	Lys	Asn	Val	Val	Tyr	260	265	270
Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	275	280	285
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Lys	Asp	Gly	Ala	290	295	300
Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	305	310	315
Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	325	330	335
Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	340	345	350
Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe	355	360	365
Pro	Arg	Thr	Leu	Ser	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	370	375	380
Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	385	390	395
Glu	Ile	Met	Gln	His	Lys	Phe	Phe	Ala	Gly	Ile	Val	Trp	Gln	Asp	Val	405	410	415
Tyr	Gly	Lys	Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	420	425	430
Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Met	Ile	Thr	435	440	445
Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Met	Asp	Cys	Val	Asp	Asn	Glu	450	455	460
Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Gly	Thr	Ala	465	470	475